IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Applicant(s)   :   BERMUDES, et al.

U.S. Serial No.:   09/645,415, now U.S. Patent No. 6,962,696, B1
                         issued November 8, 2005

Filing Date   :   August 24, 2000

For   :   COMPOSITIONS AND METHODS FOR TUMOR-TARGETED
                         DELIVERY OF EFFECTOR MOLECULES

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                         World Plaza, Suite 604
                         141-07 20th Avenue
                         Whitestone, NY 11357

                         March 10, 2006

Certificate of Corrections Branch
Commissioner for Patents
P.O. Box 1450
Alexandria, VA 22313-1450

Certificate

MAR 1 7 2006

of Correction

Sir/Madam:

COMMUNICATION TO REQUEST CERTIFICATE OF CORRECTION

Applicants hereby submit a request for a Certificate of Correction for the above-identified issued patent. In sum, Sequence Listing #34, beginning on column 105, line 67, and extending to column 111, line 66, of the issued patent, is missing its first column of letters. The error was not the result of Applicants' mistake, as it was correctly shown in the Sequence Listing, which was filed with the United States Patent & Trademark Office (USPTO) on January 7, 2002.

Form PTO/SB/44, which correctly shows Sequence Listing #34, is attached hereto as **Exhibit A**. A copy of the entire Sequence Listing, which was filed on January 7, 2002 and shown on the USPTO Patent Application Information Retrieval (PAIR) System, is

attached hereto as **Exhibit B**.   Accordingly and pursuant to 35 U.S.C. 254, Applicants respectfully request the issuance of a Certificate of Correction without charge.

If a telephone interview would be of assistance in addressing the subject matter of the present case, Applicants' undersigned attorney invites the Examiner to telephone him at the number provided below.

Pursuant to 35 U.S.C. 254, as noted *supra*, no fee is necessary in connection with the filing of this Communication.   However, if any fee is required, authorization is hereby given to charge the amount of any such fee to Deposit Account No. 50-1891.

Respectfully submitted,

Albert Wai Kit Chan

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E-mail: chank@kitchanlaw.com

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Albert Wai-Kit Chan   Date
Reg. No. 36,479

MAR 2 0 2006

UNITED STATES PATENT AND TRADEMARK OFFICE
CERTIFICATE OF CORRECTION

Page __1__ of __4__

PATENT NO. : 6,962,696 *β1*

APPLICATION NO.: 09/645,415

ISSUE DATE : November 8, 2005

INVENTOR(S) : BERMUDES, et al.

It is certified that an error appears or errors appear in the above-identified patent and that said Letters Patent is hereby corrected as shown below:

Sequence Listing 34, which begins on column 105, line 67, and extending to column 111, line 66, is missing its first column of letters and should read as follows:

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MAR 2 0 2006

PTO/SB/44 (04-05)
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Under the Paperwork Reduction Act of 1995, no persons are required to respond to a collection of information unless it displays a valid OMB control number.
(Also Form PTO-1050)

UNITED STATES PATENT AND TRADEMARK OFFICE
CERTIFICATE OF CORRECTION

Page 2 of 4

PATENT NO. : 6,962,696 *B1*

APPLICATION NO.: 09/645,415
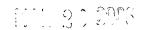
ISSUE DATE : November 8, 2005

INVENTOR(S) : BERMUDES, et al.

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Page 3 of 4

PATENT NO. : 6,962,696 B1

APPLICATION NO.: 09/645,415

ISSUE DATE : November 8, 2005

INVENTOR(S) : BERMUDES, et al.

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PATENT NO. : 6,962,696 B1

APPLICATION NO.: 09/645,415
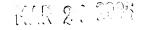
ISSUE DATE : November 8, 2005

INVENTOR(S) : BERMUDES, et al.

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MAR 20 2006

SEQUENCE LISTING

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Clairmont, C.
Lin, S.
Belcourt, M.

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-3-

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Val Leu Leu Thr His Thr Ile Ser Arg Ile Ala Val Ser Tyr Gln Thr
            100             105             110

aaa gtt aac ctg ctg agc gct atc aag tct ccg tgc cag cgt gaa act          384
Lys Val Asn Leu Leu Ser Ala Ile Lys Ser Pro Cys Gln Arg Glu Thr
            115             120             125

ccc gag ggt gca gaa gcg aaa cca tgg tat gaa ccg atc tac ctg ggt          432
Pro Glu Gly Ala Glu Ala Lys Pro Trp Tyr Glu Pro Ile Tyr Leu Gly
        130             135             140

ggc gta ttt caa ctg gag aaa ggt gac cgt ctg tcc gca gaa atc aac          480
Gly Val Phe Gln Leu Glu Lys Gly Asp Arg Leu Ser Ala Glu Ile Asn
145                 150             155             160

cgt cct gac tat cta gat ttc gct gaa tct ggc cag gtg tac ttc ggt          528
Arg Pro Asp Tyr Leu Asp Phe Ala Glu Ser Gly Gln Val Tyr Phe Gly
                165             170             175

att atc gca ctg taa                                                       543
Ile Ile Ala Leu
            180


        <210> 8
        <211> 180
        <212> PRT
        <213> Artificial Sequence

        <220>
        <223> Fusion construct

        <400> 8
Met Lys Lys Thr Ala Ile Ala Ile Ala Val Ala Leu Ala Gly Phe Ala
1               5               10              15
Thr Val Ala Gln Ala His Met Val Arg Ser Ser Ser Arg Thr Pro Ser
            20              25              30
Asp Lys Pro Val Ala His Val Val Ala Asn Pro Gln Ala Glu Gly Gln
        35              40              45
Leu Gln Trp Leu Asn Arg Arg Ala Asn Ala Leu Leu Ala Asn Gly Val
    50              55              60
Glu Leu Arg Asp Asn Gln Leu Val Val Pro Ser Glu Gly Leu Tyr Leu
65              70              75              80
Ile Tyr Ser Gln Val Leu Phe Lys Gly Gln Gly Cys Pro Ser Thr His
                85              90              95
Val Leu Leu Thr His Thr Ile Ser Arg Ile Ala Val Ser Tyr Gln Thr
            100             105             110
Lys Val Asn Leu Leu Ser Ala Ile Lys Ser Pro Cys Gln Arg Glu Thr
            115             120             125
Pro Glu Gly Ala Glu Ala Lys Pro Trp Tyr Glu Pro Ile Tyr Leu Gly
        130             135             140
Gly Val Phe Gln Leu Glu Lys Gly Asp Arg Leu Ser Ala Glu Ile Asn
145                 150             155             160
Arg Pro Asp Tyr Leu Asp Phe Ala Glu Ser Gly Gln Val Tyr Phe Gly
                165             170             175
Ile Ile Ala Leu
            180

        <210> 9
        <211> 801
        <212> DNA
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<210> Artificial Sequence

<213> Artificial Sequence

<220>
<223> Fusion construct

<221> CDS
<222> (1)...(798)

<400> 9
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atg aaa aag aca gct atc gcg att gca gtg gca ctg gct ggt ttc gct      48
Met Lys Lys Thr Ala Ile Ala Ile Ala Val Ala Leu Ala Gly Phe Ala
1               5                   10                  15

acc gta gcg cag gcc cat atg gct aac gag ctg aag cag atg cag gac      96
Thr Val Ala Gln Ala His Met Ala Asn Glu Leu Lys Gln Met Gln Asp
                20                  25                  30

aag tac tcc aaa agt ggc att gct tgt ttc tta aaa gaa gat gac agt     144
Lys Tyr Ser Lys Ser Gly Ile Ala Cys Phe Leu Lys Glu Asp Asp Ser
            35                  40                  45

tat tgg gac ccc aat gac gaa gag agt atg aac agc ccc tgc tgg caa     192
Tyr Trp Asp Pro Asn Asp Glu Glu Ser Met Asn Ser Pro Cys Trp Gln
        50                  55                  60

gtc aag tgg caa ctc cgt cag ctc gtt aga aag atg att ttg aga acc     240
Val Lys Trp Gln Leu Arg Gln Leu Val Arg Lys Met Ile Leu Arg Thr
    65                  70                  75                  80

tct gag gaa acc att tct aca gtt caa gaa aag caa caa aat att tct     288
Ser Glu Glu Thr Ile Ser Thr Val Gln Glu Lys Gln Gln Asn Ile Ser
                    85                  90                  95

ccc cta gtg aga gaa aga ggt cct cag aga gta gca gct cac ata act     336
Pro Leu Val Arg Glu Arg Gly Pro Gln Arg Val Ala Ala His Ile Thr
                100                 105                 110

ggg acc aga gga aga agc aac aca ttg tct tct cca aac tcc aag aat     384
Gly Thr Arg Gly Arg Ser Asn Thr Leu Ser Ser Pro Asn Ser Lys Asn
            115                 120                 125

gaa aag gct ctg ggc cgc aaa ata aac tcc tgg gaa tca tca agg agt     432
Glu Lys Ala Leu Gly Arg Lys Ile Asn Ser Trp Glu Ser Ser Arg Ser
        130                 135                 140

ggg cat tca ttc ctg agc aac ttg cac ttg agg aat ggt gaa ctg gtc     480
Gly His Ser Phe Leu Ser Asn Leu His Leu Arg Asn Gly Glu Leu Val
145                 150                 155                 160

atc cat gaa aaa ggg ttt tac tac atc tat tcc caa aca tac ttt cga     528
Ile His Glu Lys Gly Phe Tyr Tyr Ile Tyr Ser Gln Thr Tyr Phe Arg
                165                 170                 175

ttt cag gag gaa ata aaa gaa aac aca aag aac gac aaa caa atg gtc     576
Phe Gln Glu Glu Ile Lys Glu Asn Thr Lys Asn Asp Lys Gln Met Val
                180                 185                 190

caa tat att tac aaa tac aca agt tat cct gac cct ata ttg ttg atg     624
Gln Tyr Ile Tyr Lys Tyr Thr Ser Tyr Pro Asp Pro Ile Leu Leu Met
                195                 200                 205
```

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```
aaa agt gct aga aat agt tgt tgg tct aaa gat gca gaa tat gga ctc      672
Lys Ser Ala Arg Asn Ser Cys Trp Ser Lys Asp Ala Glu Tyr Gly Leu
    210             215             220

tat tcc atc tat caa ggg gga ata ttt gag ctt aag gaa aat gac aga      720
Tyr Ser Ile Tyr Gln Gly Gly Ile Phe Glu Leu Lys Glu Asn Asp Arg
225             230             235             240

att ttt gtt tct gta aca aat gag cac ttg ata gac atg gac cat gaa      768
Ile Phe Val Ser Val Thr Asn Glu His Leu Ile Asp Met Asp His Glu
            245             250             255

gcc agt ttt ttc ggg gcc ttt tta gtt ggc taa                         801
Ala Ser Phe Phe Gly Ala Phe Leu Val Gly
        260             265
```

<210> 10
<211> 266
<212> PRT
<213> Artificial Sequence

<220>
<223> Fusion construct

<400> 10
```
Met Lys Lys Thr Ala Ile Ala Ile Ala Val Ala Leu Ala Gly Phe Ala
1               5                   10                  15
Thr Val Ala Gln Ala His Met Ala Asn Glu Leu Lys Gln Met Gln Asp
            20                  25                  30
Lys Tyr Ser Lys Ser Gly Ile Ala Cys Phe Leu Lys Glu Asp Asp Ser
        35                  40                  45
Tyr Trp Asp Pro Asn Asp Glu Glu Ser Met Asn Ser Pro Cys Trp Gln
    50                  55                  60
Val Lys Trp Gln Leu Arg Gln Leu Val Arg Lys Met Ile Leu Arg Thr
65                  70                  75                  80
Ser Glu Glu Thr Ile Ser Thr Val Gln Glu Lys Gln Gln Asn Ile Ser
            85                  90                  95
Pro Leu Val Arg Glu Arg Gly Pro Gln Arg Val Ala Ala His Ile Thr
            100                 105                 110
Gly Thr Arg Gly Arg Ser Asn Thr Leu Ser Ser Pro Asn Ser Lys Asn
        115                 120                 125
Glu Lys Ala Leu Gly Arg Lys Ile Asn Ser Trp Glu Ser Ser Arg Ser
    130                 135                 140
Gly His Ser Phe Leu Ser Asn Leu His Leu Arg Asn Gly Glu Leu Val
145                 150                 155                 160
Ile His Glu Lys Gly Phe Tyr Tyr Ile Tyr Ser Gln Thr Tyr Phe Arg
                165                 170                 175
Phe Gln Glu Glu Ile Lys Glu Asn Thr Lys Asn Asp Lys Gln Met Val
    180                 185                 190
Gln Tyr Ile Tyr Lys Tyr Thr Ser Tyr Pro Asp Pro Ile Leu Leu Met
        195                 200                 205
Lys Ser Ala Arg Asn Ser Cys Trp Ser Lys Asp Ala Glu Tyr Gly Leu
    210             215                 220
Tyr Ser Ile Tyr Gln Gly Gly Ile Phe Glu Leu Lys Glu Asn Asp Arg
225             230                 235                 240
Ile Phe Val Ser Val Thr Asn Glu His Leu Ile Asp Met Asp His Glu
            245                 250                 255
Ala Ser Phe Phe Gly Ala Phe Leu Val Gly
        260                 265
```

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<210> 11
<211> 465
<212> DNA
<213> Artificial Sequence

<220>
<223> Fusion construct

<221> CDS
<222> (1)...(462)

<400> 11

```
atg aaa aag acg gct ctg gcg ctt ctg ctc ttg ctg tta gcg ctg act    48
Met Lys Lys Thr Ala Leu Ala Leu Leu Leu Leu Leu Leu Ala Leu Thr
1               5                   10                  15

agt gta gcg cag gcc gct cct act agc tcg agc act aag aaa act caa    96
Ser Val Ala Gln Ala Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln
            20                  25                  30

ctg caa ttg gag cat ctg ctg ctg gat ctg cag atg att ctg aat ggc    144
Leu Gln Leu Glu His Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly
        35                  40                  45

atc aat aac tac aag aac cct aag ctg act cgc atg ctg act ttc aaa    192
Ile Asn Asn Tyr Lys Asn Pro Lys Leu Thr Arg Met Leu Thr Phe Lys
    50                  55                  60

ttc tac atg ccg aaa aag gct acc gag ctc aaa cat ctc cag tgc ctg    240
Phe Tyr Met Pro Lys Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu
65                  70                  75                  80

gaa gag gaa ctg aag ccg ctg gag gaa gta ctt aac ctg gca cag tct    288
Glu Glu Glu Leu Lys Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser
                85                  90                  95

aag aac ttc cac ctg cgt ccg cgt gac ctg atc tcc aac atc aat gta    336
Lys Asn Phe His Leu Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val
            100                 105                 110

atc gtt ctt gag ctg aag gga tcc gaa acc acc ttc atg tgc gaa tac    384
Ile Val Leu Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr
        115                 120                 125

gct gac gaa acc gcc acc att gtg gag ttc ctg aac cgt tgg atc acc    432
Ala Asp Glu Thr Ala Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr
    130                 135                 140

ttt gcc caa tcg atc att agc acg tta act taa                        465
Phe Ala Gln Ser Ile Ile Ser Thr Leu Thr
145                 150
```

<210> 12
<211> 154
<212> PRT
<213> Artificial Sequence

<220>
<223> Fusion construct

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<400> 12

```
Met Lys Lys Thr Ala Leu Ala Leu Leu Leu Leu Leu Leu Ala Leu Thr
1               5                   10                  15
Ser Val Ala Gln Ala Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln
            20                  25                  30
Leu Gln Leu Glu His Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly
        35                  40                  45
Ile Asn Asn Tyr Lys Asn Pro Lys Leu Thr Arg Met Leu Thr Phe Lys
    50                  55                  60
Phe Tyr Met Pro Lys Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu
65                  70                  75                  80
Glu Glu Glu Leu Lys Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser
                85                  90                  95
Lys Asn Phe His Leu Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val
            100                 105                 110
Ile Val Leu Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr
        115                 120                 125
Ala Asp Glu Thr Ala Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr
        130                 135                 140
Phe Ala Gln Ser Ile Ile Ser Thr Leu Thr
145                 150
```

<210> 13
<211> 465
<212> DNA
<213> Artificial Sequence

<220>
<223> Fusion construct

<221> CDS
<222> (1)...(462)

<400> 13

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atg aaa cag tcg act ctg gcg ctt ctg ctc ttg ctg tta gcg ctg act     48
Met Lys Gln Ser Thr Leu Ala Leu Leu Leu Leu Leu Leu Ala Leu Thr
1               5                   10                  15

agt gtg gcc aaa gcg gct cct act agc tcg agc act aag aaa act caa     96
Ser Val Ala Lys Ala Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln
            20                  25                  30

ctg caa ttg gag cat ctg ctg ctg gat ctg cag atg att ctg aat ggc    144
Leu Gln Leu Glu His Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly
        35                  40                  45

atc aat aac tac aag aac cct aag ctg act cgc atg ctg act ttc aaa    192
Ile Asn Asn Tyr Lys Asn Pro Lys Leu Thr Arg Met Leu Thr Phe Lys
    50                  55                  60

ttc tac atg ccg aaa aag gct acc gag ctc aaa cat ctc cag tgc ctg    240
Phe Tyr Met Pro Lys Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu
65                  70                  75                  80

gaa gag gaa ctg aag ccg ctg gag gaa gta ctt aac ctg gca cag tct    288
Glu Glu Glu Leu Lys Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser
                85                  90                  95

aag aac ttc cac ctg cgt ccg cgt gac ctg atc tcc aac atc aat gta    336
Lys Asn Phe His Leu Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val
            100                 105                 110
```

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```
atc gtt ctt gag ctg aag gga tcc gaa acc acc ttc atg tgc gaa tac       384
Ile Val Leu Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr
        115                 120                 125

gct gac gaa acc gcc acc att gtg gag ttc ctg aac cgt tgg atc acc       432
Ala Asp Glu Thr Ala Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr
        130                 135                 140

ttt gcc caa tcg atc att agc acg tta act taa                          465
Phe Ala Gln Ser Ile Ile Ser Thr Leu Thr
145                     150
```

```
<210> 14
<211> 154
<212> PRT
<213> Artificial Sequence

<220>
<223> Fusion construct

<400> 14
Met Lys Gln Ser Thr Leu Ala Leu Leu Leu Leu Leu Leu Ala Leu Thr
1               5                   10                  15
Ser Val Ala Lys Ala Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln
            20              25                  30
Leu Gln Leu Glu His Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly
        35                  40                  45
Ile Asn Asn Tyr Lys Asn Pro Lys Leu Thr Arg Met Leu Thr Phe Lys
        50                  55                  60
Phe Tyr Met Pro Lys Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu
65                  70                  75                  80
Glu Glu Glu Leu Lys Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser
                85                  90                  95
Lys Asn Phe His Leu Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val
            100                 105                 110
Ile Val Leu Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr
        115                 120                 125
Ala Asp Glu Thr Ala Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr
        130                 135                 140
Phe Ala Gln Ser Ile Ile Ser Thr Leu Thr
145                     150
```

```
<210> 15
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Forward primer

<400> 15
agtctagaca atcaggcgaa gaacgg                                          26
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```
<210> 16
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Reverse primer
```

<400> 16
agccatggag tcaccctcac ttttc   25

    <210> 17
    <211> 31
    <212> DNA
    <213> Artificial Sequence

    <220>
    <223> Forward primer

    <400> 17
ggatccttaa gacccacttt cacatttaag t   31

    <210> 18
    <211> 28
    <212> DNA
    <213> Artificial Sequence

    <220>
    <223> Reverse primer

    <400> 18
ggttccatgg ttcacttttc tctatcac   28

    <210> 19
    <211> 33
    <212> DNA
    <213> Artificial Sequence

    <220>
    <223> Forward primer

    <400> 19
gtgtccatgg ggcacagcca ccgcgacttc cag   33

    <210> 20
    <211> 34
    <212> DNA
    <213> Artificial Sequence

    <220>
    <223> Reverse primer

    <400> 20
acacgagctc ctacttggag gcagtcatga agct   34

    <210> 21
    <211> 72
    <212> DNA
    <213> Artificial Sequence

    <220>
    <223> Forward primer

    <400> 21
gtgtccatgg ctcggcgggc aagtgtcggg actgaccatc atcatcatca tcatcacagc   60
caccgcgact tc   72

    <210> 22
    <211> 35
    <212> DNA

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<210> Artificial Sequence

<220>
<223> Reverse primer

<400> 22
gtgcggatcc ctacttggag gcagtcatga agctg   35

<210> 23
<211> 16
<212> PRT
<213> Homo sapiens

<400> 23
Met Ala Arg Arg Ala Ser Val Gly Thr Asp His His His His His His
1   5   10   15

<210> 24
<211> 22
<212> PRT
<213> Artificial Sequence

<220>
<223> Peptide sequence TiP 13.40

<400> 24
Ala Tyr Arg Trp Arg Leu Ser His Arg Pro Lys Thr Gly Phe Ile Arg
1   5   10   15
Val Val Met Tyr Glu Gly
            20

<210> 25
<211> 66
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide sequence encoding TiP13.40

<400> 25
gcgtaccgct ggcgcctgtc ccatcgcccg aaaaccggct ttatccgcgt ggtgatgtac   60
gaaggc   66

<210> 26
<211> 101
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide

<400> 26
gtgtactagt gtggcgcagg cggcgtaccg ctggcgcctg tcccatcgcc cgaaaaccgg   60
ctttatccgc gtggtgatgt acgaaggcta aggatccgcg c   101

<210> 27
<211> 101
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide

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<400> 27
gcgcggatcc ttagccttcg tacatcacca cgcggataaa gccggttttc gggcgatggg   60
acaggcgcca gcggtacgcc gcctgcgcca cactagtaca c   101

<210> 28
<211> 101
<212> PRT
<213> Homo sapiens

<400> 28
Met Ser Ser Ala Ala Gly Phe Cys Ala Ser Arg Pro Gly Leu Leu Phe
1   5   10   15
Leu Gly Leu Leu Leu Leu Pro Leu Val Val Ala Phe Ala Ser Ala Glu
            20   25   30
Ala Glu Glu Asp Gly Asp Leu Gln Cys Leu Cys Val Lys Thr Thr Ser
        35   40   45
Gln Val Arg Pro Arg His Ile Thr Ser Leu Glu Val Ile Lys Ala Gly
    50   55   60
Pro His Cys Pro Thr Ala Gln Leu Ile Ala Thr Leu Lys Asn Gly Arg
65   70   75   80
Lys Ile Cys Leu Asp Leu Gln Ala Pro Leu Tyr Lys Lys Ile Ile Lys
                85   90   95
Lys Leu Leu Glu Ser
            100

<210> 29
<211> 106
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide

<400> 29
cttcactagt gtggcgcagg cgaacggccg caaaatctgc ctggacctgc aggcgccgct   60
gtacaaaaaa atcatcaaaa aactgctgga aagctaagga tccgcg   106

<210> 30
<211> 106
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide

<400> 30
cgcggatcct tagctttcca gcagtttttt gatgattttt ttgtacagcg gcgcctgcag   60
gtccaggcag attttgcggc cgttcgcctg cgccacacta gtgaag   106

<210> 31
<211> 85
<212> PRT
<213> Homo sapiens

<400> 31
Ile Tyr Ser Phe Asp Gly Arg Asp Ile Met Thr Asp Pro Ser Trp Pro
1   5   10   15
Gln Lys Val Ile Trp His Gly Ser Ser Pro His Gly Val Arg Leu Val
            20   25   30
Asp Asn Tyr Cys Glu Ala Trp Arg Thr Ala Asp Thr Ala Val Thr Gly
        35   40   45

Leu Ala Ser Pro Leu Ser Thr Gly Lys Ile Leu Asp Gln Lys Ala Tyr
    50   55   60
Ser Cys Ala Asn Arg Leu Ile Val Leu Cys Ile Glu Asn Ser Phe Met
65   70   75   80
Thr Asp Ala Arg Lys
                85

<210> 32
<211> 44
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide

<400> 32
ggcttcacta gtgtggcgca ggcgatatac tcctttgatg gtcg   44

<210> 33
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide

<400> 33
cgcggatcct tacttcctag cgtctgtcat gaaactg   37

<210> 34
<211> 7117
<212> DNA
<213> E. coli

<400> 34
cccgggcact tccggggcat gagtatgtga tatccggggc tgcaccccgg accccgccaa   60
cacatcacgg gcacaaaat tttttgtggc ccgctctgcg ttttctaagt gttatccctc   120
ctgatttcta aaaatttttc cacctgaact tgacagaaaa aacgatgacg agtactttt   180
gatctgtaca taaacccagt ggttttatgt acagtattaa tcgtgtaatc aattgtttta   240
acgcttaaaa gagggaattt ttatgagcgg tggcgatgga cgcggccata acacgggcgc   300
gcatagcaca agtggtaaca ttaatggtgg cccgaccggg cttggtgtag gtggtggtgc   360
ttctgatggc tccggatgga gttcggaaaa taaccgtgg ggtggtggtt ccggtagcgg   420
cattcactgg ggtggtggtt ccggtcatgg taatggcggg gggaatggta attccggtgg   480
tggttcggga acaggcggta atctgtcagc agtagctgcg ccagtggcat ttggttttcc   540
ggcactttcc actccaggag ctggcggtct ggcggtcagt atttcagcgg gagcattatc   600
ggcagctatt gctgatatta tggctgccct gaaaggaccg tttaaatttg gtctttgggg   660
ggtggcttta tatggtgtat tgccatcaca aatagcgaaa gatgacccca atatgatgtc   720
aaagattgtg acgtcattac ccgcagatga tattactgaa tcacctgtca gttcattacc   780
tctcgataag gcaacagtaa acgtaaatgt tcgtgttgtt gatgatgtaa aagacgagcg   840
acagaatatt tcggttgttt caggtgttcc gatgagtgtt ccggtggttg atgcaaaacc   900
taccgaacgt ccgggtgttt ttacggcatc aattccaggt gcacctgttc tgaatatttc   960
agttaataac agtacgccag cagtacagac attaagccca ggtgttacaa ataatactga   1020
taaggatgtt cgcccggcag gatttactca gggtggtaat accagggatg cagttattcg   1080
attcccgaag gacagcggtc ataatgccgt atatgtttca gtgagtgatg ttcttagccc   1140
tgaccaggta aaacaacgtc aagatgaaga aaatcgccgt cagcaggaat gggatgctac   1200
gcatccggtt gaagcggctg agcgaaatta tgaacgcgcg cgtgcagagc tgaatcaggc   1260
aaatgaagat gttgccagaa atcaggagcg acaggctaaa gctgttcagg tttataattc   1320
gcgtaaaagc gaacttgatg cagcgaataa aactcttgct gatgcaatag ctgaaataaa   1380
acaatttaat cgatttgccc atgacccaat ggctggcggt cacagaatgt ggcaaatggc   1440
cgggcttaaa gcccagcggg cgcagacgga tgtaaataat aagcaggctg catttgatgc   1500
tgctgcaaaa gagaagtcag atgctgatgc tgcattgagt tctgctatgg aaagcaggaa   1560
gaagaaagaa gataagaaaa ggagtgctga aaataattta aacgatgaaa agaataagcc   1620

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cagaaaggt tttaaagatt acgggcatga ttatcatcca gctccgaaaa ctgagaatat    1680
taaagggctt ggtgatctta agcctgggat accaaaaaca ccaaagcaga atggtggtgg    1740
aaaacgcaag cgctggactg gagataaagg gcgtaagatt tatgagtggg attctcagca    1800
tggtgagctt gaggggtatc gtgccagtga tggtcagcat cttggctcat ttgaccctaa    1860
aacaggcaat cagttgaaag gtccagatcc gaaacgaaat atcttttgaga    1920
ggaagttatg ggacttaaat ttggtttgat aaaagtacag aagattttaa    1980
gggtgaggag tattcaaaag attttggaga tgacggttca gttatggaaa gtctaggtgt    2040
gcctttttaag gataatgtta ataacgttg ctttgatgtt atagctgaat gggtacctt    2100
gctacaacca tactttaatc atcaaattga tatttccgat aatgagtatt ttgtttcgtt    2160
tgattatcgt gatggtgatt ggtgatcaaa tattatcagg gatgagttga tatacgggct    2220
tctagtgttc atggatgaac gctggagcct ccaaatgtag aaatgttata ttttttattg    2280
agttcttggt tataattgct ccgcaatgat ttaaataagc attatttaaa acattctcag    2340
gagaggtgaa ggtggagcta aaaaaaagta ttggtgatta cactgaaacc gaattcaaaa    2400
aatttattga agacatcatc aattgtgaag gtgatgaaaa aaaacaggat gataacctcg    2460
agtattttat aaatgttact gagcatccta gtggttctga tctgatttat tacccagaag    2520
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<220>
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<210> 36
<211> 35
<212> DNA
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<220>
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<400> 36
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<220>
<223> Forward primer

-15-

<400> 37

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    <210> 38
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    <212> DNA
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    <220>
    <223> Forward primer

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    <211> 67
    <212> DNA
    <213> Artificial Sequence

    <220>
    <223> Reverse primer

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gacgcac   67

    <210> 43
    <211> 71
    <212> DNA

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<213> Artificial Sequence

<220>
<223> Forward primer

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<213> Artificial Sequence

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<210> 46
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<220>
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<400> 46
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<210> 47
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<212> DNA
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<220>
<223> Forward primer

<400> 47
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<210> 48
<211> 33
<212> DNA
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<220>
<223> Reverse primer

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<400> 48
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<212> DNA
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gaagataccc cgccgggccc gtccaccgtg tttcgcccgc cg   102

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<211> 103
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide

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ccagcgggcg ggaggaggtc ggcgggcgaa acacggtgga cgg   103

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<220>
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<210> 53
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<220>
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<212> DNA
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<220>
<223> Oligonucleotide

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<212> DNA
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<220>
<223> Oligonucleotide

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cgcatgaacg cgctgcagga agataccccg ccgggccc                               98

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<220>
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<211> 551
<212> DNA
<213> Bacteriophage

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<223> n=a, c, g, or t

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nagacc atg gct tat ggc aga aaa aaa aga aga cag aga aga aga atg         48
       Met Ala Tyr Gly Arg Lys Lys Arg Arg Gln Arg Arg Arg Met
        1               5                  10

aac gcg ctg cag gaa gat acc ccg ccg ggc ccg tcc acc gtg ttt cgc        96
Asn Ala Leu Gln Glu Asp Thr Pro Pro Gly Pro Ser Thr Val Phe Arg
 15              20                  25                  30

ccg ccg acc tcc tcc cgc ccg ctg gaa acc ccg cat tgc cgc gaa atc       144
Pro Pro Thr Ser Ser Arg Pro Leu Glu Thr Pro His Cys Arg Glu Ile
             35                  40                  45

cgc atc ggc atc gcg ggc atc acc atc acc ctg tcc ctg tgc ggc tgc       192
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MAR 20 2006
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Arg Ile Gly Ile Ala Gly Ile Thr Ile Thr Leu Ser Leu Cys Gly Cys
         50                      55                  60

gcg aac gcg cgc gcg ccg acc ctg cgc tcc gcg acc gcg gat aac tcc      240
Ala Asn Ala Arg Ala Pro Thr Leu Arg Ser Ala Thr Ala Asp Asn Ser
     65                  70                  75

gaa aac acc ggc ttt aaa aac gtc ccg gat ctg cgc acc gat cag ccg      288
Glu Asn Thr Gly Phe Lys Asn Val Pro Asp Leu Arg Thr Asp Gln Pro
     80                  85                  90

aaa ccg ccg tcc aaa aaa cgc tcc tgc gat ccg tcc gaa tat cgc gtc      336
Lys Pro Pro Ser Lys Lys Arg Ser Cys Asp Pro Ser Glu Tyr Arg Val
 95                  100                 105                 110

tcc gaa ctg aaa gaa tcc ctg atc acc acc acc ccg tcc cgc ccg cgc      384
Ser Glu Leu Lys Glu Ser Leu Ile Thr Thr Thr Pro Ser Arg Pro Arg
             115                 120                 125

acc gcc cgc cgc tgc atc cgc ctc tgaaagcttg gctgttttgg cggatgagag     438
Thr Ala Arg Arg Cys Ile Arg Leu
                 130

aagattttca gcctgataca gattaaatca gaacgcagaa gcggtctgat aaaacagaat     498
ttgcctggcg gcagtagcgc ggtggtccca cctgacccca tgccgaactc aga            551
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        <210> 58
        <211> 134
        <212> PRT
        <213> Bacteriophage

        <400> 58
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 1               5                  10                  15
Leu Gln Glu Asp Thr Pro Pro Gly Pro Ser Thr Val Phe Arg Pro Pro
             20                  25                  30
Thr Ser Ser Arg Pro Leu Glu Thr Pro His Cys Arg Glu Ile Arg Ile
         35                  40                  45
Gly Ile Ala Gly Ile Thr Ile Thr Leu Ser Leu Cys Gly Cys Ala Asn
     50                  55                  60
Ala Arg Ala Pro Thr Leu Arg Ser Ala Thr Ala Asp Asn Ser Glu Asn
 65                  70                  75                  80
Thr Gly Phe Lys Asn Val Pro Asp Leu Arg Thr Asp Gln Pro Lys Pro
                 85                  90                  95
Pro Ser Lys Lys Arg Ser Cys Asp Pro Ser Glu Tyr Arg Val Ser Glu
             100                 105                 110
Leu Lys Glu Ser Leu Ile Thr Thr Thr Pro Ser Arg Pro Arg Thr Ala
         115                 120                 125
Arg Arg Cys Ile Arg Leu
     130
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        <210> 59
        <211> 444
        <212> DNA
        <213> Bacteriophage

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        <221> modified_base
        <222> (1)...(1)
        <223> n=a, c, g, or t

        <221> CDS

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<222> (7)...(427)

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        Met Ala His His His His His His Tyr Gly Arg Lys Lys Arg
        1   5   10

cgt cag cgc cgt cgc atg aac gcg ctg cag gaa gat acc ccg ccg ggc   96
Arg Gln Arg Arg Arg Met Asn Ala Leu Gln Glu Asp Thr Pro Pro Gly
15   20   25   30

ccg tcc acc gtg ttt cgc ccg ccg acc tcc tcc cgc ccg ctg gaa acc   144
Pro Ser Thr Val Phe Arg Pro Pro Thr Ser Ser Arg Pro Leu Glu Thr
                35   40   45

ccg cat tgc cgc gaa atc cgc atc ggc atc gcg ggc atc acc atc acc   192
Pro His Cys Arg Glu Ile Arg Ile Gly Ile Ala Gly Ile Thr Ile Thr
            50   55   60

ctg tcc ctg tgc ggc tgc gcg aac gcg cgc gcg ccg acc ctg cgc tcc   240
Leu Ser Leu Cys Gly Cys Ala Asn Ala Arg Ala Pro Thr Leu Arg Ser
        65   70   75

gcg acc gcg gat aac tcc gaa aac acc ggc ttt aaa aac gtc ccg gat   288
Ala Thr Ala Asp Asn Ser Glu Asn Thr Gly Phe Lys Asn Val Pro Asp
    80   85   90

ctg cgc acc gat cag ccg aaa ccg ccg tcc aaa aaa cgc tcc tgc gat   336
Leu Arg Thr Asp Gln Pro Lys Pro Pro Ser Lys Lys Arg Ser Cys Asp
95   100   105   110

ccg tcc gaa tat cgc gtc tcc gaa ctg aaa gaa tcc ctg atc acc acc   384
Pro Ser Glu Tyr Arg Val Ser Glu Leu Lys Glu Ser Leu Ile Thr Thr
                115   120   125

acc ccg tcc cgc ccg cgc acc gcc cgc cgc tgc atc cgc ctc t   427
Thr Pro Ser Arg Pro Arg Thr Ala Arg Arg Cys Ile Arg Leu
        130   135   140

gaaagcttgg ctgtttt   444

<210> 60
<211> 140
<212> PRT
<213> Bacteriophage

<400> 60
Met Ala His His His His His His Tyr Gly Arg Lys Lys Arg Arg Gln
1   5   10   15
Arg Arg Arg Met Asn Ala Leu Gln Glu Asp Thr Pro Pro Gly Pro Ser
            20   25   30
Thr Val Phe Arg Pro Pro Thr Ser Ser Arg Pro Leu Glu Thr Pro His
        35   40   45
Cys Arg Glu Ile Arg Ile Gly Ile Ala Gly Ile Thr Ile Thr Leu Ser
    50   55   60
Leu Cys Gly Cys Ala Asn Ala Arg Ala Pro Thr Leu Arg Ser Ala Thr
65   70   75   80
Ala Asp Asn Ser Glu Asn Thr Gly Phe Lys Asn Val Pro Asp Leu Arg
            85   90   95
Thr Asp Gln Pro Lys Pro Pro Ser Lys Lys Arg Ser Cys Asp Pro Ser
        100   105   110

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Glu Tyr Arg Val Ser Glu Leu Lys Glu Ser Leu Ile Thr Thr Thr Pro
    115                 120                 125
Ser Arg Pro Arg Thr Ala Arg Arg Cys Ile Arg Leu
    130                 135                 140


    <210> 61
    <211> 1565
    <212> DNA
    <213> Salmonella


    <400> 61
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cgcgcagtca tcaccgcaac gcaaatgatg gagtcgatga tcaccaaccc gatgccgacc     180
cgtgcggaag tgatggacgt ggcgaacgcc gtcctggatg gcacggatgc ggttatgctg     240
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tgcctggggcg cagaaaaaat ccccagcatc aatgtgtcta aacaccgtct cgacgtgcag     360
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ccttaattaa ccccgcatgc ggggggccat ataggccggg gatttaaatg caaacgtccg     780
ccgaaacgcc gacgcactgt gttccagata tagtcaaaaa ccggattacc ctgattatga     840
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cagccatgcg gtacgagaaa aatgactttt cgtcgttac gacgcatctc ctcgataatc     960
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tgatc                                                                1565
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